

Sequence Listing.ST25.txt  
SEQUENCE LISTING

<110> Novo Nordisk Pharmaceuticals, Inc.  
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Susanne, Bang  
Olesen, Ole H  
Petersen, Lars C  
  
<120> Kunitz-Type Sequences and Polypeptides  
  
<130> 6297.204-US  
  
<140> To be assigned  
<141> 2003-11-25  
  
<150> Danish Application No. PA 2001 00859  
<151> 2001-05-31  
  
<150> US 60/303,180  
<151> 2001-07-05  
  
<150> PCT/DK02/00372  
<151> 2002-05-31  
  
<160> 34  
  
<170> PatentIn version 3.2  
  
<210> 1  
<211> 58  
<212> PRT  
<213> Artificial  
  
<220>  
<223> Amino acid sequence of human wild type HK1-18

<400> 1  
Tyr Pro Val Arg Cys Leu Leu Pro Ser Ala His Gly Ser Cys Ala Asp  
1 5 10 15

Trp Ala Ala Arg Trp Tyr Phe Val Ala Ser Val Gly Gln Cys Asn Arg  
20 25 30

Phe Trp Tyr Gly Gly Cys His Gly Asn Ala Asn Asn Phe Ala Ser Glu  
35 40 45

Gln Glu Cys Met Ser Ser Cys Gln Gly Ser  
50 55

<210> 2  
<211> 51  
<212> PRT  
<213> Artificial  
  
<220>  
<223> Synthetic

Sequence Listing.ST25.txt

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<220>
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<222> (2)..(2)
<223> X in position 2 is Ala, Val, Leu, Ser, Thr, Asn, Lys, Glu, Gln,
      Arg, Phe, Tyr, Met, or is absent

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<221> MISC_FEATURE
<222> (3)..(3)
<223> X in position 3 is Ala, Val, Leu, Ser, Thr, Asp, Glu, Gln, Phe,
      Met, or is absent

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> X in position 4 is Gly, Ala, Leu, Ser, Asp, Lys, Glu, Gln, Pro,
      or is absent

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> X in position 5 is Ala, Val, Leu, Glu, Ser, Asn, Lys, Glu, Tyr,
      Met, Pro, or is absent

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> X in position 6 is Ala, Val, Leu, Ser, Asp, Asn, Lys, Glu, Arg,
      Tyr, Met, or is absent

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<222> (7)..(7)
<223> X in position 7 is Ala, Val, Thr, Asp, Lys, Glu, Gln, Arg, His,
      Tyr, Pro, or is absent

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<222> (8)..(8)
<223> X in position 8 is Gly, Asp, or is absent

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> X in position 9 is Leu, Glu, Ser, Thr, Asn, Gln, Arg, Pro, or is
      absent

<220>
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<222> (11)..(11)
<223> X in position 11 is Gly, Ala, Leu, Ser, Thr, Asn, Lys, Glu, Gln,
      Arg, Met, or is absent

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<222> (12)..(12)
<223> X in position 12 is Gly, Ala, Thr, Asp, Glu, His, or is absent

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> X in position 13 is Leu, Glu, Ser, Asn, Glu, Arg, Phe, Trp, Tyr,
      Met, or is absent
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Sequence Listing.ST25.txt

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<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> X in position 14 is Ala, Val, Leu, Glu, Thr, Glu, Phe, Met, or is
absent

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> X in position 15 is Ala, Val, Leu, Glu, Ser, Thr, Asn, Lys, Glu,
Gln, Pro, or is absent

<220>
<221> MISC_FEATURE
<222> (16)..(16)
<223> X in position 16 is Leu, Lys, Arg, His, or is absent

<220>
<221> MISC_FEATURE
<222> (17)..(17)
<223> X in position 17 is Phe, Trp, Tyr, or is absent

<220>
<221> MISC_FEATURE
<222> (18)..(18)
<223> X in position 18 is Ala, His, Phe, Trp, Tyr, or is absent

<220>
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<222> (19)..(19)
<223> X in position 19 is Phe, Tyr, or is absent

<220>
<221> MISC_FEATURE
<222> (20)..(20)
<223> X in position 20 is Val, Ser, Asp, Asn, Arg, or is absent

<220>
<221> MISC_FEATURE
<222> (21)..(21)
<223> X in position 21 is Gly, Ala, Leu, Glu, Ser, Asn, Lys, Phe, Pro,
or is absent

<220>
<221> MISC_FEATURE
<222> (22)..(22)
<223> X in position 22 is Val, Leu, Ser, Thr, Asn, Lys, Glu, Gln, Arg,
Phe, Tyr, or is absent

<220>
<221> MISC_FEATURE
<222> (23)..(23)
<223> X in position 23 is Ala, Val, Leu, Glu, Ser, Thr, Asp, Asn, Lys,
Glu, Arg, Tyr, or is absent

<220>
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<222> (24)..(24)
<223> X in position 24 is Gly, Asn, Lys, Glu, Gln, Arg, Tyr, Met, or is
absent
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<220>

Sequence Listing.ST25.txt

<221> MISC\_FEATURE  
<222> (25)..(25)  
<223> X in position 25 is Ala, Leu, Glu, Ser, Thr, Lys, Glu, Gln, Arg, His, or is absent

<220>  
<221> MISC\_FEATURE  
<222> (27)..(27)  
<223> X in position 27 is Ala, Val, Ser, Thr, Asp, Asn, Lys, Glu, Gln, Arg, His, or is absent

<220>  
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<222> (28)..(28)  
<223> X in position 28 is Ala, Leu, Ser, Thr, Asn, Lys, Glu, Gln, Arg, Met, Pro, or is absent

<220>  
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<222> (30)..(30)  
<223> X in position 30 is Ala, Val, Leu, Glu, Thr, Lys, Gln, Phe, Trp, Pro, or is absent

<220>  
<221> MISC\_FEATURE  
<222> (31)..(31)  
<223> X in position 31 is Ser, Phe, Tyr, or is absent

<220>  
<221> MISC\_FEATURE  
<222> (32)..(32)  
<223> X in position 32 is Gly, Ser, Thr, Arg, or is absent

<220>  
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<222> (35)..(35)  
<223> X in position 35 is Gly, Leu, Asp, Asn, Glu, Gln, Arg, His, Tyr, Met, or is absent

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<221> MISC\_FEATURE  
<222> (36)..(36)  
<223> X in position 36 is Gly, Ala, Arg, or is absent

<220>  
<221> MISC\_FEATURE  
<222> (37)..(37)  
<223> X in position 37 is Ser, Asp, Asn, Lys, or is absent

<220>  
<221> MISC\_FEATURE  
<222> (38)..(38)  
<223> X in position 38 is Gly, Ala, Ser, Asp, Asn, Lys, Glu, Gln, Arg, or is absent

<220>  
<221> MISC\_FEATURE  
<222> (40)..(40)  
<223> X in position 40 is Ser, Asn, Lys, Arg, or is absent

<220>  
<221> MISC\_FEATURE  
<222> (41)..(41)

Sequence Listing.ST25.txt

<223> X in position 41 is Phe, Tyr, or is absent

<220>

<221> MISC\_FEATURE

<222> (42)..(42)

<223> X in position 42 is Gly, Ala, Val, Leu, Thr, Asp, Asn, Lys, Glu, Gln, Arg, His, Tyr, Pro, or is absent

<220>

<221> MISC\_FEATURE

<222> (43)..(43)

<223> X in position 43 is Ser, Thr, Asp, Asn, Glu, Arg, or is absent

<220>

<221> MISC\_FEATURE

<222> (44)..(44)

<223> X in position 44 is Ala, Leu, Lys, Glu, Gln, Arg, Trp, or is absent

<220>

<221> MISC\_FEATURE

<222> (45)..(45)

<223> X in position 45 is Ala, Asp, Lys, Glu, Gln, or is absent

<220>

<221> MISC\_FEATURE

<222> (46)..(46)

<223> X in position 46 is Ala, Ser, Thr, Asp, Asn, Lys, Glu, Gln, Tyr, or is absent

<220>

<221> MISC\_FEATURE

<222> (48)..(48)

<223> X in position 48 is Leu, Ile, Glu, Asp, Lys, Glu, Gln, Arg, Met, or is absent

<220>

<221> MISC\_FEATURE

<222> (49)..(49)

<223> X in position 49 is Gly, Ala, Leu, Ser, Thr, Asp, Asn, Lys, Glu, Gln, Arg, or is absent

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<222> (50)..(50)

<223> X in position 50 is Ala, Ser, Thr, Val, Glu, Lys, Arg, Phe, Met, or is absent

<220>

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<222> (50)..(50)

<223> X in position 50 is Ala, Ser, Thr, Val, Glu, Lys, Arg, Phe, Met, or is absent

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Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa  
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Phe Xaa Xaa Xaa  
20 25 30

Sequence Listing.ST25.txt

Gly Cys Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa  
35 40 45

Xaa Xaa Cys  
50

<210> 3  
<211> 174  
<212> DNA  
<213> Homo sapiens

<400> 3  
taccccggtgc ggtgcctgct gcccagtgcc catggctctt gcgcagactg ggctgcccc 60  
tggtaacctcg ttgcctctgt gggccaatgt aaccgcttct ggtatggcgg ctgcatggc 120  
aatgccaata actttgcctc ggagcaagag tgcatgagca gctgccaggg atct 174

<210> 4  
<211> 58  
<212> PRT  
<213> Homo sapiens

<400> 4

Tyr Pro Val Arg Cys Leu Leu Pro Pro Ala Thr Gly Pro Cys Lys Ala  
1 5 10 15

Arg Ile Ile Arg Trp Tyr Phe Val Ala Ser Val Gly Gln Cys Asn Arg  
20 25 30

Phe Val Tyr Gly Gly Cys Arg Gly Asn Ala Asn Asn Phe Ala Ser Glu  
35 40 45

Gln Glu Cys Met Ser Ser Cys Gln Gly ser  
50 55

<210> 5  
<211> 58  
<212> PRT  
<213> Homo sapiens

<400> 5

Tyr Pro Val Arg Cys Leu Leu Pro Pro Ala Thr Gly Pro Cys Arg Ala  
1 5 10 15

Arg Ile Ile Arg Trp Tyr Phe Val Ala Ser Val Gly Gln Cys Asn Arg  
20 25 30

Phe Val Tyr Gly Gly Cys Arg Gly Asn Ala Asn Asn Phe Ala Ser Glu  
35 40 45

Sequence Listing.ST25.txt

Gln Glu Cys Met Ser Ser Cys Gln Gly Ser  
50 55

<210> 6  
<211> 58  
<212> PRT  
<213> Homo sapiens

<400> 6

Tyr Pro Val Arg Cys Leu Leu Pro Pro Ala Thr Gly Ser Cys Lys Ala  
1 5 10 15

Trp Ala Ala Arg Trp Tyr Phe Val Ala Ser Val Gly Gln Cys Asn Arg  
20 25 30

Phe Trp Tyr Gly Gly Cys His Gly Asn Ala Asn Asn Phe Ala Ser Glu  
35 40 45

Gln Glu Cys Met Ser Ser Cys Gln Gly Ser  
50 55

<210> 7  
<211> 58  
<212> PRT  
<213> Homo sapiens

<400> 7

Tyr Pro Val Arg Cys Leu Leu Pro Pro Ala Thr Gly Pro Cys Lys Ala  
1 5 10 15

Arg Ala Ala Arg Trp Tyr Phe Val Ala Ser Val Gly Gln Cys Asn Arg  
20 25 30

Phe Val Tyr Gly Gly Cys His Gly Asn Ala Asn Asn Phe Ala Ser Glu  
35 40 45

Gln Glu Cys Met Ser Ser Cys Gln Gly Ser  
50 55

<210> 8  
<211> 18  
<212> DNA  
<213> Homo sapiens

<400> 8  
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18

<210> 9  
<211> 40  
<212> DNA

Sequence Listing.ST25.txt

<213> Homo sapiens

<400> 9  
ccttgatagg cccagccggc ctaccccgta cggtgcctgc 40

<210> 10

<211> 39

<212> DNA

<213> Homo sapiens

<400> 10  
ggatgtcaag cggccgcaga tccctggcag ctgctcatg 39

<210> 11

<211> 25

<212> DNA

<213> Homo sapiens

<400> 11  
ctgcagaagc accatcaggt tggtg 25

<210> 12

<211> 27

<212> DNA

<213> Homo sapiens

<400> 12  
tctcttcctcc aatctctcag ccatggc 27

<210> 13

<211> 47

<212> DNA

<213> Homo sapiens

<400> 13  
catggcttag agattggaga agagataccc cgtgcgggtgc ctgctgc 47

<210> 14

<211> 43

<212> DNA

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caggctgatc tagacttaag atccctggca gctgctcatg cac 43

<210> 15

<211> 25

<212> DNA

<213> Homo sapiens

<400> 15  
caggaattcc attcaagaat agttc 25

<210> 16

<211> 30

<212> DNA

Sequence Listing.ST25.txt

<213> Homo sapiens

<400> 16

ccgtagtcat caatttattt tacataacac

30

<210> 17

<211> 44

<212> DNA

<213> Homo sapiens

<400> 17

ctttggctaa cgtcgccatg gctgagagat tggagaagag atac

44

<210> 18

<211> 42

<212> DNA

<213> Homo sapiens

<400> 18

gggcagcagg caccgcacgg ggtatctttt ctccaatctc tc

42

<210> 19

<211> 42

<212> DNA

<213> Homo sapiens

<400> 19

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<213> Homo sapiens

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44

<210> 21

<211> 44

<212> DNA

<213> Homo sapiens

<400> 21

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44

<210> 22

<211> 45

<212> DNA

<213> Homo sapiens

<400> 22

catgacagcc gccataccag aagcggtac attggccac agagg

45

<210> 23

<211> 46

<212> DNA

Sequence Listing.ST25.txt

<213> Homo sapiens

<400> 23

ctggtatggc ggctgtcatg gcaatgc当地 taactttgcc tcggag

46

<210> 24

<211> 40

<212> DNA

<213> Homo sapiens

<400> 24

cagctgctca tgcactcttg ctccgaggca aagttattgg

40

<210> 25

<211> 40

<212> DNA

<213> Homo sapiens

<400> 25

caagagtgc当地 tgagcagctg ccagggatct taagtctaga

40

<210> 26

<211> 33

<212> DNA

<213> Homo sapiens

<400> 26

cacggcttta gtttctagac ttaagatccc tgg

33

<210> 27

<211> 42

<212> DNA

<213> Homo sapiens

<400> 27

ccgtgcggtg cctgctgccc cctgccactg gcccttgcaa ag

42

<210> 28

<211> 44

<212> DNA

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<400> 28

gaagtaccag cgggcagccc tggcttgca agggccagtg gcag

44

<210> 29

<211> 45

<212> DNA

<213> Homo sapiens

<400> 29

catgacagcc gccatacacg aagcggttac attggccac agagg

45

<210> 30

<211> 46

<212> DNA

Sequence Listing.ST25.txt

<213> Homo sapiens

<400> 30  
cgtgtatggc ggctgtcatg gcaatgc当地 taactttgcc tcggag 46

<210> 31  
<211> 419  
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<213> Artificial

<220>  
<223> Nucleotide sequence encoding the 212L-HKI18 fusion polypeptide

<400> 31  
gaattccatt caagaatagt tcaaacaaga agattacaaa ctatcaattt catacacaat 60  
ataaacgacc aaaagaatga aggctgtttt cttggtttg tccttgatcg gattctgctg 120  
ggcccaacca gtcactggcg atgaatcatc tggttagatt ccgaaagagt ctctgatcat 180  
cgctgaaaac accactttgg ctaacgtcgc catggctgag agattggaga agagataccc 240  
cgtgcggtgc ctgctgccc gtgcccattt ctcttgcgc gactgggctg cccgctggta 300  
cttcgttgcc tctgtgggccc aatgttaaccg cttctggat ggcggctgcc atggcaatgc 360  
caataactt gcctcgagc aagagtgc gaggcagctc caggatctt aagtctaga 419

<210> 32  
<211> 111  
<212> PRT  
<213> Artificial

<220>  
<223> Amino acid sequence of the 212L-HKI18 fusion polypeptide

<400> 32

Met Lys Ala Val Phe Leu Val Leu Ser Leu Ile Gly Phe Cys Trp Ala  
1 5 10 15

Gln Pro Val Thr Gly Asp Glu Ser Ser Val Glu Ile Pro Glu Glu Ser  
20 25 30

Leu Ile Ile Ala Glu Asn Thr Thr Leu Ala Asn Val Ala Met Ala Glu  
35 40 45

Arg Leu Glu Lys Arg Tyr Pro Val Arg Cys Leu Leu Pro Ser Ala His  
50 55 60

Gly Ser Cys Ala Asp Trp Ala Ala Arg Trp Tyr Phe Val Ala Ser Val  
65 70 75 80

Gly Gln Cys Asn Arg Phe Trp Tyr Gly Gly Cys His Gly Asn Ala Asn  
85 90 95

Sequence Listing.ST25.txt

Asn Phe Ala Ser Glu Gln Glu Cys Met Ser Ser Cys Gln Gly Ser  
100 105 110

<210> 33  
<211> 111  
<212> PRT  
<213> Artificial

<220>  
<223> Amino acid sequence of the 212L-HK18-1 fusion polypeptide  
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Met Lys Ala Val Phe Leu Val Leu Ser Leu Ile Gly Phe Cys Trp Ala  
1 5 10 15

Gln Pro Val Thr Gly Asp Glu Ser Ser Val Glu Ile Pro Glu Glu Ser  
20 25 30

Leu Ile Ile Ala Glu Asn Thr Thr Leu Ala Asn Val Ala Met Ala Glu  
35 40 45

Arg Leu Glu Lys Arg Tyr Pro Val Arg Cys Leu Leu Pro Pro Ala Thr  
50 55 60

Gly Ser Cys Lys Ala Trp Ala Ala Arg Trp Tyr Phe Val Ala Ser Val  
65 70 75 80

Gly Gln Cys Asn Arg Phe Trp Tyr Gly Gly Cys His Gly Asn Ala Asn  
85 90 95

Asn Phe Ala Ser Glu Gln Glu Cys Met Ser Ser Cys Gln Gly Ser  
100 105 110

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Met Lys Ala Val Phe Leu Val Leu Ser Leu Ile Gly Phe Cys Trp Ala  
1 5 10 15

Gln Pro Val Thr Gly Asp Glu Ser Ser Val Glu Ile Pro Glu Glu Ser  
20 25 30

Leu Ile Ile Ala Glu Asn Thr Thr Leu Ala Asn Val Ala Met Ala Glu  
35 40 45

Sequence Listing.ST25.txt

Arg Leu Glu Lys Arg Tyr Pro Val Arg Cys Leu Leu Pro Pro Ala Thr  
50 55 60

Gly Pro Cys Lys Ala Arg Ala Ala Arg Trp Tyr Phe Val Ala Ser Val  
65 70 75 80

Gly Gln Cys Asn Arg Phe Val Tyr Gly Gly Cys His Gly Asn Ala Asn  
85 90 95

Asn Phe Ala Ser Glu Gln Glu Cys Met Ser Ser Cys Gln Gly Ser  
100 105 110